LUD 5615 (09905230)

GP 11642/BOX
seq

P#13

## IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

| | | |
|---|---|---|
| Applicant(s) | : | JAGER, et al. |
| Serial No. | : | 09/451,739 |
| Filed | : | November 30, 1999 |
| For | : | ISOLATED NUCLEIC ACID MOLECULES ENCODING CANCER ASSOCIATED ANTIGENS, THE ANTIGENS PER SE, AND USES THEREOF |
| Group Art Unit | : | 1642 |
| Examiner | : | G. Nickol |

February 2, 2001

Hon. Commissioner of Patents
and Trademarks
Washington, D.C. 20231

### LETTER

In response to the office action of January 28, please replace the paper copy of the sequence listing and CRF of same with the attached.

The undersigned hereby declares that to the best of his knowledge, the information presented on the attached paper copy of sequence listing and computer readable form thereof are identical to each other and to information set forth in the above referenced patent application as filed. No new matter is believed presented.

Respectfully submitted,

FULBRIGHT & JAWORSKI L.L.P.

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715658.1

<110> Jager, Dirk
      Scanlan, Matthew
      Gure, Ali
      Jager, Elke
      Knuth, Alexander
      Old, Lloyd
      Chen, Yao-tseng

<120> Isolated Nucleic Acid Molecules Encoding Cancer Associated Antigens,
      the Antigens per se, and Uses Thereof

<130> LUD 5615

<140> 09/451,739

<141> 1999-11-30

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Lys Ala Leu Glu Leu Lys Asn Glu Gln Thr Leu Arg Ala Asp Gln Met
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          85              90              95

Gln Glu Leu Gly Asp Glu Lys Ile Gln Ile Val Ser Gln Met Val Glu
          100             105             110

Leu Val Glu Asn Arg Thr Arg Gln Val Asp Ser His Val Glu Leu Phe
          115             120             125

Glu Ala Gln Gln Glu Leu Gly Asp Thr Val Gly Asn Ser Gly Lys Val
    130             135             140

Gly Ala Asp Arg Pro Asn Gly Asp Ala Val Ala Gln Ser Asp Lys Pro
145             150             155             160

Asn Ser Lys Arg Ser Arg Arg Gln Arg Asn Asn Glu Asn Arg Glu Asn
              165             170             175

Ala Ser Ser Asn His Asp His Asp Asp Gly Ala Ser Gly Thr Pro Lys
```

```
          180                    185                    190
Glu Lys Lys Ala Lys Thr Ser Lys Lys Lys Arg Ser Lys Ala Lys
        195                200                205

Ala Glu Arg Glu Ala Ser Pro Ala Asp Leu Pro Ile Asp Pro Asn Glu
        210                215                220

Pro Thr Tyr Cys Leu Cys Asn Gln Val Ser Tyr Gly Glu Met Ile Gly
225                230                235                240

Cys Asp Asn Asp Glu Cys Pro Ile Glu Trp Phe His Phe Ser Cys Val
            245                250                255

Gly Leu Asn His Lys Pro Lys Gly Lys Trp Tyr Cys Pro Lys Cys Arg
            260                265                270

Gly Glu Asn Glu Lys Thr Met Asp Lys Ala Leu Glu Lys Ser Lys Lys
        275                280                285

Glu Arg Ala Tyr Asn Arg
    290            294
```

**UNITED STAT◯ DEPARTMENT OF COMMERCE**
**Patent and Trademark Office**
Address:  COMMISSIONER OF PATENTS AND TRADEMARKS
Washington, D.C. 20231

| APPLICATION NO. | FILING DATE | FIRST NAMED INVENTOR | ATTORNEY DOCKET NO. |
|---|---|---|---|
| 09/451,739 | 11/30/99 | JAGER | b  LUD-5615 |

┌─────────────────────────────┐
┌─                           ─┐  | **EXAMINER** |
  024972           HM02/0130A   └─────────────────────────────┘
  FULBRIGHT & JAWORSKI, LLP       NICKOL, G
  666 FIFTH AVE
  NEW YORK NY 10103-3198
└─                           ─┘

| ART UNIT | PAPER NUMBER |
|---|---|
| 1642 | 19 |

**DATE MAILED:**   01/30/01

Please find below and/or attached an Office communication concerning this application or proceeding.

Commissioner of Patents and Trademarks

PTO-90C (Rev. 2/95)                                    2 - Mail Copy

DEA/FCE-1994

| SERIAL NUMBER | FILING DATE | FIRST NAMED APPLICANT | | ATTORNEY DOCKET NO. |
|---|---|---|---|---|
| 09/451739 | | | | |

| EXAMINER | |
|---|---|
| Gary B. Nickol Ph.D. | |
| ART UNIT | PAPER NUMBER |
| 1642 | |

DATE MAILED:

## Please find below a communication from the EXAMINER in charge of this application

Commissioner of Patents

The communication filed on 01/02/01 is not fully responsive for the reasons set forth on the attached Notice to Comply with the Sequence Rules or CRF Diskette Problem Report.

Since the response appears to be _bona fide_, but through an apparent oversight or inadvertence failed to provide a complete response, APPLICANT IS GIVEN ONE MONTH FROM THE DATE OF THIS LETTER WITHIN WHICH TO COMPLY WITH THE SEQUENCE RULES, 37 CFR 1.821-1.825. Failure to comply with these requirements will result in ABANDONMENT of the application under 37 CFR 1.136 (g). Extensions of time may be obtained by filing a petition accompanied by the extension fee under the provisions of 37 CFR 1.136. In no case may an applicant extend the period for response beyond the six month statutory period. Direct the response to the undersigned. Applicant is requested to return a copy of the attached Notice to Comply with the response.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Gary Nickol, Ph.D. whose telephone number is (703) 305-7143. The examiner can normally be reached on Monday through Friday from 830am to 630pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Anthony Caputa, can be reached on (703) 308-3995. The fax phone number for this Group is (703) 305-3014 or (703) 308-4242.

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the Group receptionist whose telephone number is (703) 308-0196.

Gary B. Nickol Ph.D.
January 26, 2001

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FEB 13 2001

TECH CENTER 1600/2900

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES
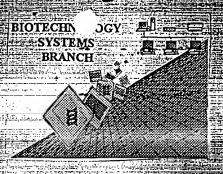
Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

[X] 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).

[ ] 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).

[ ] 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).

[ ] 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."

[X] 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).

[ ] 6. The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).

[ ] 7. Other: _____

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**FEB 13 2001**

**TECH CENTER 1600/2900**

## Applicant Must Provide:

[X] An initial or <u>substitute</u> computer readable form (CRF) copy of the "Sequence Listing".

[X] An initial or <u>substitute</u> paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.

[X] A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216
For CRF Submission Help, call (703) 308-4212
PatentIn Software Program Support
     Technical Assistance.........................................703-287-0200
     To Purchase PatentIn Software........................703-306-2600

**PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR REPLY**

# RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY SYSTEMS BRANCH

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/451,739B_

Source: _1642_

Date Processed by STIC: _1/2/2001_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

## Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

**ERROR DETECTED · SUGGESTED · CORRECTION**            SERIAL NUMBER: 09/457,939 B

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics          The number/text at the end of each line "wrapped" down to the next line.
                                  This may occur if your file was retrieved in a word processor after creating it.
                                  Please adjust your right margin to .3, as this will prevent "wrapping".

_____ Wrapped Aminos             The amino acid number/text at the end of each line "wrapped" down to the next line.
                                  This may occur if your file was retrieved in a word processor after creating it.
                                  Please adjust your right margin to .3, as this will prevent "wrapping".

_____ Incorrect Line Length      The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid    The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
       Numbering                 between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII                This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
                                  Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length          Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
                                  As per the rules, each n or Xaa can only represent a single residue.
                                  Please present the maximum number of each residue having variable length and
                                  indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"  A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
                                  sequence(s) _____. Normally, PatentIn would automatically generate this section from the
                                  previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
                                  to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
                                  sections for Artificial or Unknown sequences.

8 _____ Skipped Sequences        Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
       (OLD RULES)               (2) INFORMATION FOR SEQ ID NO:X:
                                  (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
                                  (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
                                  This sequence is intentionally skipped

                                  Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences        Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
       (NEW RULES)               <210> sequence id number
                                  <400> sequence id number
                                  000

10 _____ Use of n's or Xaa's     Use of n's and/or Xaa's have been detected in the Sequence Listing.
        (NEW RULES)              Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
                                  In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism    Sequence(s) _____ are missing this mandatory field or its response.
        (NEW RULES)

12 _____ Use of <220>Feature     Sequence(s) _____ are missing the <220>Feature and associated headings.
        (NEW RULES)              Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
                                  Please explain source of genetic material in <220> to <223> section.
                                  (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
                                  file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
                                  Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIPE
FEB 0 6 2001
PATENT & TRADEMARK OFFICE

3. Nickol

O!PE JC25
FEB 0 6 2001

1642

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/451,739B

DATE: 01/02/2001
TIME: 11:02:39

Input Set : A:\ES.txt
Output Set: N:\CRF3\01022001\I451739B.raw

Does Not Comply
Corrected Diskette Needed

see item 5 on
Error
Summary
Sheet

```
1  <110> APPLICANT: Jager, Dirk
2          Scanlan, Matthew
3          Gure, Ali
4          Jager, Elke
5          Knuth, Alexander
6          Old, Lloyd
7          Chen, Yao-tseng
9  <120> TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer Associated
10         Antigens,
11         the Antigens per se, and Uses Thereof
13 <130> FILE REFERENCE: LUD 5515
15 <140> CURRENT APPLICATION NUMBER: 09/451,739B
17 <141> CURRENT FILING DATE: 1999-11-30
19 <160> NUMBER OF SEQ ID NOS: 19
```

ERRORED SEQUENCES

```
520 <210> SEQ ID NO: 16
521 <211> LENGTH: (513)  512 shown (next page)
522 <212> TYPE: PRT
524 <213> ORGANISM: Homo sapiens
524 <400> SEQUENCE: 16
525 Met Lys Val Ser Ile Pro Thr Lys Ala Leu Glu Glu Met Asp Met Gln
526 1               5                   10                  15
528 Thr Phe Lys Ala Glu Pro Pro Glu Lys Pro Ser Ala Phe Glu Pro Ala
529                 20                  25                  30
531 Ile Glu Met Glu Lys Ser Val Pro Asn Lys Ala Leu Glu Leu Lys Asn
532             35                  40                  45
534 Glu Glu Thr Leu Arg Ala Asp Glu Ile Leu Pro Ser Glu Ser Lys Glu
535         50                  55                  60
537 Lys Asp Tyr Glu Glu Ser Ser Trp Asp Ser Glu Ser Leu Cys Glu Thr
538 65                  70                  75                  80
540 Val Ser Glu Lys Asp Val Cys Leu Pro Lys Ala Thr His Gln Lys Glu
541                 85                  90                  95
543 Ile Asp Lys Ile Asn Gly Lys Leu Glu Glu Ser Pro Asp Asn Asp Gly
544                 100                 105                 110
547 Phe Leu Lys Ala Pro Cys Arg Met Lys Val Ser Ile Pro Thr Lys Ala
548             115                 120                 125
550 Leu Glu Leu Met Asp Met Gln Thr Phe Lys Ala Glu Pro Pro Glu Lys
551         130                 135                 140
553 Pro Ser Ala Phe Glu Pro Ala Ile Glu Met Gln Lys Ser Val Pro Asn
554 145                 150                 155                 160
556 Lys Ala Leu Glu Leu Lys Asn Glu Gln Thr Leu Arg Ala Asp Gln Met
557                 165                 170                 175
559 Phe Pro Ser Glu Ser Lys Glu Lys Lys Val Glu Glu Asn Ser Trp Asp
560                 180                 185                 190
```

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FEB 13 2001
TECH CENTER 1600/2900

RAW SEQUENCE LISTING     DATE: 01/02/2001
PATENT APPLICATION: US/09/451,739B     TIME: 11:02:39

Input Set : A:\ES.txt
Output Set: N:\CRF3\01022001\I451739B.raw

```
     562 Ser Glu Ser Leu Arg Glu Thr Val Ser Gln Lys Asp Val Cys Val Pro
     563         195                 200                 205
     565 Lys Ala Thr His Gln Lys Glu Met Asp Lys Ile Ser Gly Lys Leu Glu
     566     210                 215                 220
     568 Asp Ser Thr Ser Leu Ser Lys Ile Leu Asp Thr Val His Ser Cys Glu
     569 225                 230                 235                 240
     571 Arg Ala Arg Glu Leu Gln Lys Asp His Cys Glu Gln Arg Thr Gly Lys
E--> 572         245 245             250 250             255 255
     574 Met Glu Gln Met Lys Lys Lys Phe Cys Val Leu Lys Lys Lys Leu Ser
E--> 575         260 260             265 265             270 270
     577 Glu Ala Lys Glu Ile Lys Ser Gln Leu Gln Asn Glu Lys Val Lys Trp
E--> 578     275                 280                 285
     580 Glu Gln Glu Leu Cys Ser Val Arg Leu Thr Leu Asn Gln Glu Glu Gln
E  > 581 290                 295                 300                 305
     583 Lys Arg Arg Asn Ala Asp Ile Leu Asn Glu Lys Ile Arg Glu Glu Leu
E--> 584             310                 315                 320
     586 Gly Arg Ile Glu Glu Gln His Arg Lys Glu Leu Glu Val Lys Gln Glu
E--> 587         325                 330                 335
     589 Leu Glu Gln Ala Leu Arg Ile Thr Asp Ile Glu Leu Lys Ser Val Asn
E--> 590         340                 345                 350
     592 Ser Asn Leu Asn Glu Val Ser His Thr His Glu Asn Glu Asn Tyr Leu
E--> 593     355                 360                 365
     595 Leu His Glu Asn Cys Met Leu Lys Lys Glu Ile Ala Met Leu Lys Leu
E--> 596 370                 375                 380                 385
     598 Glu Ile Ala Thr Leu Lys His Gln Tyr Gln Glu Lys Glu Asn Lys Tyr
E--> 599             390                 395                 400
     601 Phe Glu Asp Ile Lys Ile Leu Lys Glu Lys Asn Ala Glu Leu Gln Met
E--> 602         405                 410                 415
     604 Thr Leu Lys Leu Lys Glu Glu Ser Ile Thr Lys Arg Ala Ser Gln Tyr
E--> 605     420                 425                 430
     607 Ser Gly Gln Leu Lys Val Leu Ile Ala His Asn Thr Met Leu Thr Ser
E--> 608     435                 440                 445
     610 Lys Leu Lys Glu Lys Gln Asp Lys Glu Ile Leu Gln Ala Gln Ile Glu
E--> 611 450                 455                 460                 465
     613 Ser His Asp Pro Arg Leu Ala Ser Ala Val Gln Asp His Asp Gln Ile
E--> 615             470                 475                 480
     617 Val Thr Ser Arg Lys Ser Gln Glu Pro Ala Phe His Ile Ala Gly Asp
E--> 618         485                 490                 495
     620 Ala Cys Leu Gln Arg Lys Met Asn Val Asp Val Ser Ser Thr Asp Ile
E--> 621         500                 505                 510
```

*misaligned amino acid numbers (see item 4 on Error Summary Sheet)*

*see next page for more errors*

07/451,939B    7

<210> 1
<211> 1533
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
<222> 235
<400> 1

```
ggttttccac gttggacaag tgcggctcgg cggccagcgg agcgcgcccc ttcccgctgc   60
ccgctccgct cctctcttct acccagccca gtgggcgagt gggcagcggc ggccgcggcg  120
ctgggccctc tcccgccggt gtgtgcgcgc tcgtacgcgc ggcccccggc gccagccccg  180
ccgcctgaga gggggcctgc gccgccggcc ggggcgtgcg cccgggagcc accgccaccg  240
cggcccgcgc cctcaggcgc tggggtcccc gcggacccgg aggcggcgga cgggctcggc  300
agatgtagcc gccgggccga agcaggagcc ggcggggggg cgccgggaga gcgagggctt  360
tgcattttgc agtgctattt tttgaggggg cgggagggtg gaggaagtcg gaaagccgcg  420
ccgagtcgcc ggggacctcc ggggtgaacc atgttgagtc ctgccaacgg ggagcagctc  480
cacctggtga actatgtgga ggactacctg gactccatcg agtccctgcc tttcgacttg  540
cagagaaatg tctcgctgat gcgggagatc gacgcgaaat accaagagat cctgaaggag  600
ctagacgagt gctacgagcg cttcagtcgc gagacagacg gggcgcagaa gcggcggatg  660
ctgcactgtg tgcagcgcgc gctgatccgc agccaggagc tgggcgacga gaagatccag  720
atcgtgagcc agatggtgga gctggtggag aaccgcacgc ggcaggtgga cagccacgtg  780
gagctgttcg aggcgcagca ggagctgggc gacacagcgg gcaacagcgg caaggctggc  840
gcggacaggc ccaaaggcga ggcggcagcg caggctgaca agcccaacag caagcgctca  900
cggcggcagc gcaacaacga gaaccgtgag aacgcgtcca gcaaccacga ccacgacgac  960
ggcgcctcgg gcacacccaa ggagaagaag gccaagacct ccaagaagaa gaagcgctcc 1020
aaggccaagg cggagcgaga ggcgtcccct gccgacctcc ccatcgaccc caacgaaccc 1080
acgtactgtc tgtgcaacca ggtctcctat ggggagatga tcggctgcga caacgacgag 1140
tgccccatcg agtggttcca cttctcgtgc gtggggctca atcataaacc caagggcaag 1200
tggtactgtc ccaagtgccg gggggagaac gagaagacca tggacaaagc cctggagaaa 1260
tccaaaaaag agagggctta caacaggtag tttgtggaca ggcgcctggt gtgaggagga 1320
caaaataaac cgtgtattta ttacattgct gcctttgttg aggtgcaagg agtgtaaaat 1380
gtatattttt aaagaatgtt agaaaaggaa ccattccttt cataggatg gcagtgattc 1440
tgtttgcctt ttgttttcat tggtacacgt gtaacaagaa agtggtctgt ggatcagcat 1500
tttagaaact acaaatatag gtttgattca aca                               1533
```

FYI:

VERIFICATION SUMMARY     DATE: 01/02/2001
PATENT APPLICATION: U 09/451,739    TIME: 11:02:40

Input Set : A:\ES.txt
Output Set: N:\CRF3\01022001\I451739B.raw

```
L:26  M:283 W: Missing Blank Line separator, <220> field identifier
L:29  M:283 W: Missing Blank Line separator, <400> field identifier
L:36  M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:36  M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:1
L:87  M:283 W: Missing Blank Line separator, <400> field identifier
L:133 M:283 W: Missing Blank Line separator, <220> field identifier
L:134 M:283 W: Missing Blank Line separator, <400> field identifier
L:167 M:283 W: Missing Blank Line separator, <400> field identifier
L:203 M:283 W: Missing Blank Line separator, <400> field identifier
L:264 M:283 W: Missing Blank Line separator, <220> field identifier
L:265 M:283 W: Missing Blank Line separator, <400> field identifier
L:314 M:283 W: Missing Blank Line separator, <400> field identifier
L:367 M:283 W: Missing Blank Line separator, <400> field identifier
L:390 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:8
L:390 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8
L:390 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:8
L:399 M:283 W: Missing Blank Line separator, <400> field identifier
L:407 M:283 W: Missing Blank Line separator, <400> field identifier
L:415 M:283 W: Missing Blank Line separator, <400> field identifier
L:423 M:283 W: Missing Blank Line separator, <400> field identifier
L:431 M:283 W: Missing Blank Line separator, <400> field identifier
L:439 M:283 W: Missing Blank Line separator, <400> field identifier
L:450 M:283 W: Missing Blank Line separator, <400> field identifier
L:505 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:15
L:505 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15
L:505 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:15
L:509 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:15
L:509 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15
M:440 Repeated in SeqNo 15
L:513 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:15
L:513 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15
L:515 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:15
L:515 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15
L:517 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:15
L:517 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15
L:524 M:283 W: Missing Blank Line separator, <400> field identifier
L:572 M:342 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
M:552 Repeated in SeqNo 16
L:621 M:252 E: No. of Seq. differs. <211>LENGTH:Input:513 Found:512 SEQ:16
L:628 M:283 W: Missing Blank Line separator, <400> field identifier
L:636 M:283 W: Missing Blank Line separator, <400> field identifier
L:641 M:283 W: Missing Blank Line separator, <400> field identifier
```